Figure 1

Figure 1 (cont. 1)

torA/s.m. :		
torA/s.c :		
torA/s.p. :		

Figure 1 (.cont. 2)

```
                    2100        2120        2140        2160        2180        2200
torA/S.m. : TTGGTTGCAGTCATGCCATCCAGAGACAAACGTTTACACTCGCGAGATGTGTGGAGAATACCCGCGAGACTTACGGACGTCGAGTCAATGGCCGTGTATATCAGCCCTGTCGACGCAAAAGCACGT
torA/S.c  : TTGGTTCCAGTCCATGCCACCCAGAGACAAACCTTTACACTCGCGAGATGTGTGGAGAATACCCGCGAGACTTACGGACGTCGAGTCAATGGCCGTGTATATCAGCCCTGTCGACGCAAAAGCGCGC
torA/S.p. : GTGGTTGCAATCTGGCCATCCGGAATCACCGGTTACACTCACAAATGTGTGAGTGAGTCAAACCTACACAGTTAATGCTCGCGAACCTGTGTATATTAGCCGTGGAAGATGCTAAAACCCGT
                                                                                                          2340

                    2220        2240        2260        2280        2300        2320
torA/S.m. : GGCATCAAAGATGGCGATATAGTCGGAGTCTTTAACGACCGTGGCCAACTGTTGGCCGGGGTGGTGTGTCGTATCGGACAACTTCCCTAAAGGGGATTGTGCGAATTCACGAAGCGCGTCGTATGGGCCAGTAG
torA/S.c  : GGCATAAAGATGGCGATATAGTCGGAGTCTTTAACGACCGTGGCCAACTGTTGGCCGGGGTGGTGTGTCGTATCGGACAACTTCCCTACTGGTATTGTGCGGATTCACGAAGGCGCATGGTATGGGCCAGTAG
torA/S.p. : GGCAATTAAAGATGGCGATATCGTGCGGGTCTTTAACGACCGAGTCAAACTGTTAGCGCTGGACCGGCCAGTGTATCGGATCGTTCCCTAAAGGTGCGTTAGTGGCAATGCATGGAAGTGAAGGTCATGTATGCCCAGTGG
                                                                                                          2460

                    2360        2380        2400        2420        2440
torA/S.m. : GTAAAGATGGTAGCACTGAAGGTGGTGCTGAAGTCGGCGCCCTGTGTAGTTATGCGGATCCTAACACCCTCACTTAGACATAGGCACCTCTAAACTTGCCCAAGCTTGCTCAGCCTATACTTGCTTAGT
torA/S.c  : GTAAAGATGGTAGCACTGAAGGTGGTGCTGAAGTCGGCGCCCTGTGTCAGTTATGGCGGATCCTAACACCCTCACTTAGACATAGGCACCTCTAAACTTGCCCAAGCTTGCTCAGCCTATACTTGCTTAGT
torA/S.p. : GTAAAGATGGTAGCACTGAAGGTGGGGCTTGAAGTCGGCGGCCCTGTGTCGCCGGATCGTTCCCTAAAGGTGCGTTAGTCAAGCTGAGTCAAGCTTATGGTTCCTAACCTTAGTTGGCTTCCTCAGCCTTAGTATGCTGCTTATACATGTCTCTGCT
                                                                                                          2560

                    2480        2500        2520        2540
torA/S.m. : CGAGTTTGAAAAATACCAAGGCAAAGTGCCTAAGCTCAGCTCCTTCGATGGCCCGATCGGAAGTCGAAATC------------------------------------------------
torA/S.c  : CGAGTTTGAGAAATACCAAGGCAAAGTGCCTAAGGTCCTTCAGTCCTTCGATGGCCCCTATCGAAGTCGAAATC-----------------------------------
torA/S.p. : TGAGTTTGAAAAATACCAAGGTAAAGACACCTAAAGGTTAGCTCCTTCGATGGTCCTTCGATGGGTCCTTATCGAAGTTGAAATC-----------------------------------
```

Figure 2

torA/Shewanella C

```
ATGAACAGAAGAGACTTTTTAAAGGGTATCGCCTCATCCTCTTTCGTTGTCTTAGGTGGCAG
CTCAGTGTTAGCGCCCTTAAATGCCTTAGCCAAAACGGGCATCAATGAAGACGAATGGCTAA
CCACAGGTTCACACTTCGGCGCCTTTAAAATGAAGCGCAAAAACGGCGTCATTGCCGAAGTG
AAACCCTTCGACTTAGATAAGTATCCAACGGATATGATTAACGGCATCCGCGACATGGTCTA
CAATCCATCGCGTGTACGTTACCCTATGGTGCGCTTAGATTTTTTACTCAAAGGTCATAAGA    i
GTAATACCCATCAACGGGGTGATTTCCGCTTTGTTCGTGTAACATGGGACAAGGCATTAACA
CTGTTTAAGCATTCATTAGATGAAGTCCAAACCCAATACGGTCCATCAGGTCTGCATGCGGG
TCAAACTGGTTGGCGCGCCACGGGTCAACTGCATTCCAGCACGAGTCATATGCAACGTGCGG
TGGGGATGCACGGCAACTATGTGAAGAAATCGGCGACTACTCCACAGGTGCAGGCCAAACA
ATTCTGCCCTACGTGTTAGGTTCAACCGAAGTGTATGCCCAAGGCACTTCATGGCCGCTGAT
CTTAGAACACAGCGACACTATCGTGCTCTGGTCGAACGATCCGTACAAGAACCTGCAAGTGG
GTTGGAATGCGGAAACCCATGAATCTTTTGCTTATCTTGCGCAGTTAAAAGAGAAAGTGAAG
CAAGGCAAGATCCGTGTTATCAGTATCGACCCTGTGGTGACTAAGACCCAAGCCTATTTGGG
CTGTGAGCAACTCTACGTTAACCCACAGACAGACGTGACTTTAATGCTGGCCATCGCCCACG
AGATGATCAGCAAAAAGCTCTACGACGATAAATTTATCCAAGGCTACAGCTTAGGTTTTGAA
GAGTTTGTGCCCTATGTGATGGGTACTAAAGATGGCGTAGCCAAAACCCCAGAATGGGCCGC
GCCTATCTGTGGTGTTGAAGCCCATGTTATCCGCGACTTGGCTAAAACCTTAGTCAAGGGCC
GCACTCAGTTCATGATGGGCTGGTGTATCCAGCGCCAGCAACACGGCGAACAACCCTATTGG
ATGGCGGCGGTACTGGCGACCATGATCGGCCAAATCGGTCTACCCGGTGGTGGCATCAGTTA
TGGTCACCACTACTCGAGTATCGGCGTGCCTTCATCGGGTGCCGCGGCGCCAGGTGCTTTCC
CCCGTAACTTGGACGAAAATCAAAAGCCACTATTTGATAGCTCAGACTTCAAGGGCGCGAGC
AGCACAATTCCGGTTGCCCGCTGGATTGATGCGATTCTCGAACCTGGTAAAACCATTGATGC
TAACGGCTCGAAAGTGGTTTATCCCGATATCAAGATGATGATTTTCTCGGGTAATAATCCTT
GGAACCATCACCAAGACAGAAACCGTATGAAGCAAGCCTTCCATAAGCTTGAGTGTGTGGTC
ACTGTTGATGTGAACTGGACGGCAACTTGCCGCTTCTCGGATATCGTACTACCCGCTTGTAC
TACCTATGAGCGCAACGATATCGACGTTTACGGCGCCTATGCTAACCGCGGTATTTTAGCCA
TGCAGAAAATGGTTGAGCCACTGTTTGATAGCTTGTCGGATTTTGAAATTTTCACTCGCTTT
GCCGCCGTACTTGGTAAAGAGAAAGAATACACCCGTAACATGGGCGAAATGGAGTGGCTAGA
AACCCTCTATAACGAATGTAAAGCCGCCAACGCGGGCAAGTTTGAGATGCCTGACTTTGCGA
CTTTCTGGAAACAAGGTTATGTGCATTTTGGTGACGGTGAACTCTGGACGCGCCATGCAGAC
TTTAGAAACGATCCTGAAATCAATCCACTAGGCACGCCTTCAGGTTTGATTGAAATCTTTAG
CCGTAAGATTGATCAATTCGGTTACGATGACTGTAAAGGTCACCCAACTTGGATGGAGAAAA
CCGAGCGTAGCCATGGCGGCCCTGGTTCTGACAAGCATCCGATTTGGTTGCAGTCATGCCAC
CCAGACAAACGCTTACACTCGCAAATGTGTGAGTCGCGAGAATACCGCGAGACCTACGCAGT
CAATGGCCGTGAGCCTGTGTATATCAGCCCTGTCGACGCAAAAGCGCGCGGCATAAAAGATG
GCGATATAGTGCGAGTCTTTAACGACCGTGGCCAACTGTTGGCGGGTGCAGTGGTATCGGAC
AACTTCCCTACTGGTATTGTGCGGATTCACGAAGGCGCATGGTATGGGCCAGTAGGTAAAGA
TGGTAGCACTGAAGGTGGGGCTGAAGTCGGCGCCCTGTGCAGTTATGGCGATCCTAACACCC
TCACTTTAGACATAGGCACATCTAAACTTGCCCAAGCTTGCTCAGCCTATACTTGCTTAGTC
GAGTTTGAGAAATACCAAGGCAAAGTGCCTAAGGTCAGCTCCTTCGATGGCCCTATCGAAGT
CGAAATC
```

Figure 3

Photobacterium phosphoreum

5′ACAATACTGAAAGATTGTAAGACATTGATATGGTGGTCAAATGATCCGATT
AAAAACAGTCAGGTTGGCTGGCAGTGTGAGACTCATGGTTCTTATGAGTATTA
TGCGCAATTAAAGCAGAAGGTCGCAGATGGTGGGATCCGTATGATCTCGGTCG
ATCCTGTAGTGTCGAAATCGCAAAAATATTTTAACTGTGAGCACCAATACGTC
AATCCTCAAACTGACGTTCCTTTCATGCTTGCTATTGCGCATACATTGTATAA
AGAAGATCTGTACGATAAACAATTTCTGGAAACTTACACTTTAGGCTTCAATG
AATTCTTGCCTTACTTATTGGGTACAGGCAAAGATAAAATAGCCAAAACGCCA
GAATGGGCAGAGCCAATTTGTGGCGTTAAAGCAGAGGCTATTCGAGAATTTGC
TCGCGGATTAGTTAAAAACCGTACGATGATAATGTTTGGTTGGGCTGTACAGC
GTCAACAACACGGTGAGCAGCCTTATTGGATGGGAGCAGTGCTGGCTTCGATG
TTAGGCCAAATAGGCTTACCTGGTGGAGGGATTTCCTATTCTCACTTTTACAG
TGGCGTTGGGTTACCTTTCAGTACTGCAGCTGGGCCGGGGGGATTTCCGCGTA
ATGTTGATGAAGGCCAACAGCCGATTTGGAATAATAACGATTTTAAAGGCTAC
AGTTCGACAATTCCGGTCGCAAGATGGATTGATGCGATCATGGAACCAGGTAA
AAAAATTCAATATAACGGCGCTAATGTGGTGTTGCCTGATATTAAGATGATGG
TCTTTAGTGGTTGTAATCCGTGGAATCATCATCAACAACGTAATCGTATGAAA
CAAGCATTTAGAAAGCTGCAAACCGTGGTTAATATTGATTATACATGGACACC
AACCTGTCGTTTTCCGATATTGTATTACCTGCTTGTACCCAATTTGAGCGTA
GTGATTTAGATCAATATGGTACTTATTCAACTAGCGGTATTTTAGCGATGCAT
AAGCTAATTGATCCGCTTTATCAATCAAAAACAGACTTTCAGATATTTACTGA
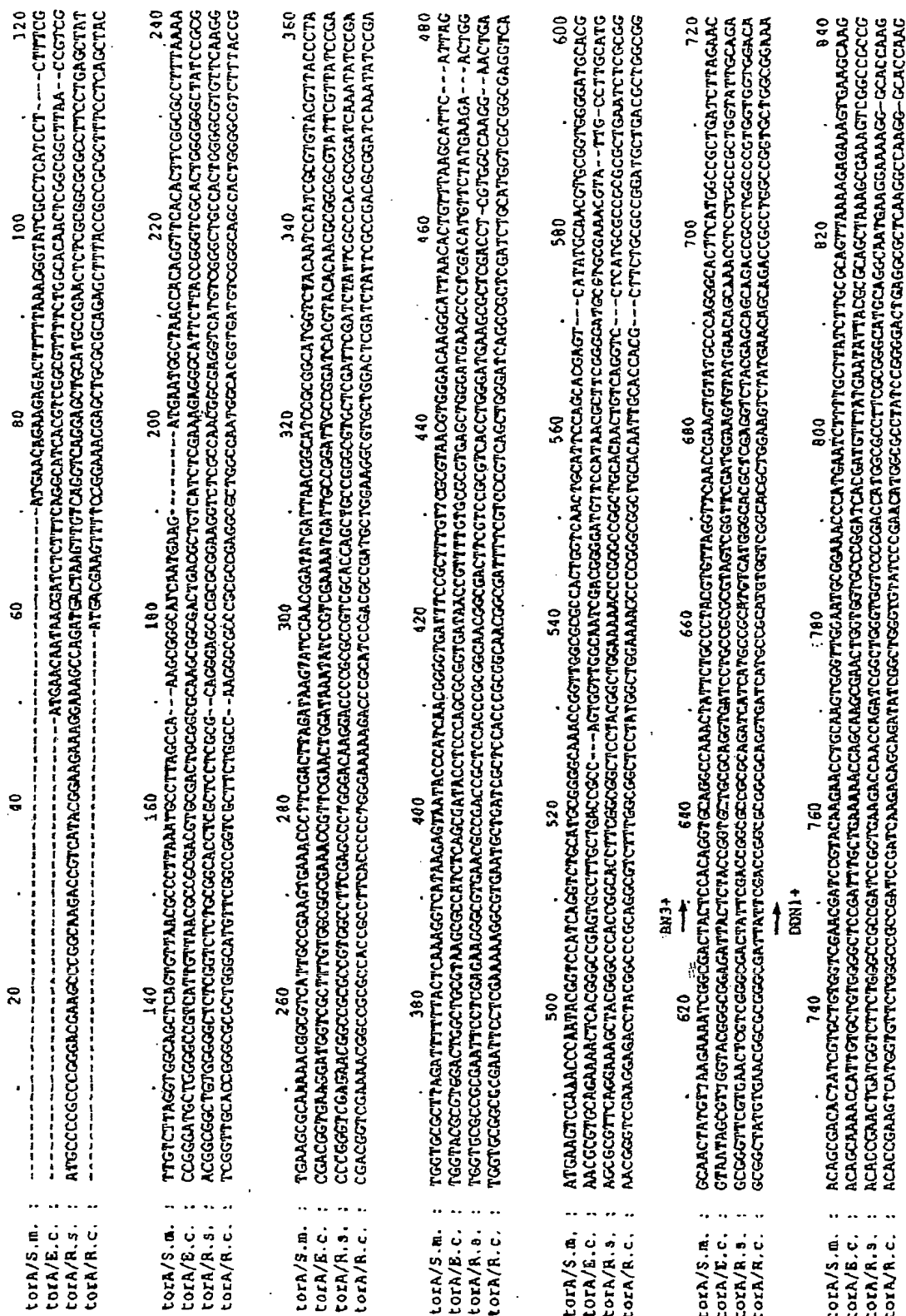ATTAACCGAACGCTTTGGGAAA 3′

Figure 4

Figure 4 (cont. 1)

torA/S.m.
torA/E.c.
torA/R.s.
torA/R.c.

Figure 4 (cont. 2)

Figure 4 (cont. 3)

```
                    2540       2560       2580       2600       2620       2640
torA/S.m. : AGCCTATACTTGCTTAGTCGAGTTTGAAAAATACCAAGCCAAAGTGCCTAAGTCCTTCGATGGCCGATCGAAGTCGAAATC----------------------------
torA/E.c. : TGGCACACTACGCTGGTGGAAATTGAGAAGTACAACGGAACAGTGGACCAGGTTAACGGCGTTAACGGCCAGTGGCGGATGGGTGGCGCCAGTGGCGAATATGTTCCCGCGTCGGCAGGTGAA
torA/R.s. : CGGCCAGAGACCATCCTCCGCGGATGTCGAAAAATATGCGGGCGCGGCCGGTGACGGTGTTCGACACGCCGAGGGACCC------------------------------------
torA/R.c. : TGGTCAGACCGGTGCTGCCCGAGGTCGAGAAATACACCCGCCCCCCGTCACCCTGACCGGCTTTGTCGGCGCGAGGCGGTCGAA----------------------------------

torA/S.m. : ---
torA/E.c. : ATCA
torA/R.s. : ---
torA/R.c. : ---
```

Figure 5

Salmonella typhimurium

```
5'ATGAAACAGGTGGTGTCGCCGCAGTTTGAAGCGCGTAACGACTTTGATATT
TTCCGCGATCTCTGCCGACGCTTTAACCGTGAAGCGGCATTCACGGAAGGTCT
TGATGAAATGGGCTGGCTGAAACGCATCTGGCAGGAAGGGAGCCAGCAGGGAA
AAGGTCGCGGTATCCACTTACCGATTTTCGAGGTGTTCTGGAATCAACAGGAG
TACATCGAGTTTGATCATCCGCAGATGTTTGTACGCCATCAGGCTTTCCGTGA
AGATCCGGACCTGGAGCCGTTGGGCACGCCAAGCGGTTTGATCGAGATTTACT
CCAAAACCATCGCCGACATGCAATACGACGATGGTCAGGGCCATCCCATGTGG
TTCGAAAAAATCGAACGCTCGCATGGCGGGCCGGGATCGCAGCGCTGGCCGCT
GCACTTACAATCCGTCCACCCTGATTTCCGTCTGCATTCCCAACTGTTGCGAG
TC  3'
```

Figure 6

TorA/Shewanella C

```
MNRRDFLKGIASSSFVVLGGSSVLAPLNALAKTGINEDEWLTTGSHFGAFKMK
RKNGVIAEVKPFDLDKYPTDMINGIRDMVYNPSRVRYPMVRLDFLLKGHKSNT
HQRGDFRFVRVTWDKALTLFKHSLDEVQTQYGPSGLHAGQTGWRATGQLHSST
SHMQRAVGMHGNYVKKIGDYSTGAGQTILPYVLGSTEVYAQGTSWPLILEHSD
TIVLWSNDPYKNLQVGWNAETHESFAYLAQLKEKVKQGKIRVISIDPVVTKTQ
AYLGCEQLYVNPQTDVTLMLAIAHEMISKKLYDDKFIQGYSLGFEEFVPYVMG
TKDGVAKTPEWAAPICGVEAHVIRDLAKTLVKGRTQFMMGWCIQRQQHGEQPY
WMAAVLATMIGQIGLPGGGISYGHHYSSIGVPSSGAAAPGAFPRNLDENQKPL
FDSSDFKGASSTIPVARWIDAILEPGKTIDANGSKVVYPDIKMMIFSGNNPWN
HHQDRNRMKQAFHKLECVVTVDVNWTATCRFSDIVLPACTTYERNDIDVYGAY
ANRGILAMQKMVEPLFDSLSDFEIFTRFAAVLGKEKEYTRNMGEMEWLETLYN
ECKAANAGKFEMPDFATFWKQGYVHFGDGELWTRHADFRNDPEINPLGTPSGL
IEIFSRKIDQFGYDDCKGHPTWMEKTERSHGGPGSDKHPIWLQSCHPDKRLHS
QMCESREYRETYAVNGREPVYISPVDAKARGIKDGDIVRVFNDRGQLLAGAVV
SDNFPTGIVRIHEGAWYGPVKDGSTEGGAEVGALCSYGDPNTLTLDIGTSKL
AQACSAYTCLVEFEKYQGKVPKVSSFDGPIEVEI
```

Figure 7

```
TorA/P.p. :        TILKDCKTLIWWSNDPIKNSQVGWQCETHGSYEYYAQLKQKVA
TorA/S.m. :        GTSWPLILEHSDTIVLWSNDPYKNLQVGWNAETHESFAYLAQLKEKVK
TorA/E.c. :        QTSWPLVLQNSKTIVLWGSDLLKNQQANWWCPDHDVYEYYAQLKRKSA
DorA/R.s. :        QTAWPVVVENTDLMVFWAADPMKTNEIGWVIPDHGAYAGMKALKEK--


TorA/P.p. :        DGGIRMISVDPVVSKSQKYFN---CEHQYVNPQTDVPFMLAIAHTLYKED
TorA/S.m. :        QGKIRVISIDPVVTKTQAYLG---CEQLYVNPQTDVTLMLAIAHEMISKK
TorA/E.c. :        AGEIEVISIDPVVTSTHEYLGGEHVKHIAVNPQTDVPLQLALAHTLYSEN
DorA/R.s. :        -G-TRVICINPVRTETADYFG---ADVVSPRPQTDVALMLGMAHTLYSED


TorA/P.p. :        LYDKQFLETYTLGFNEFLPYLLGTGKDKIAKTPEWAEPICGVKAEAIREF
TorA/S.m. :        LYDDKFIQGYSLGFEEFVPYVMGT-KDGVAKTPEWAAPICGVEAHVIRDL
TorA/E.c. :        LYDKNFLANYCVGFEEFLPYLLGE-KDGQPKDAAWAEKLSGIDAETIRGL
DorA/R.s. :        LHDKDFLENCTTGFDLFAAYLTGE-SDGTPKTAEWAAEICGLPAEQIREL


TorA/P.p. :        ARGLVKNRTMIMFGWAVQRQQHGEQPYWMGAVLASMLGQIGLPGGGISYS
TorA/S.m. :        AKTLVKGRTQFMMGWCIQRQQHGEQPYWMAAVLATMIGQIGLPGGGISYG
TorA/E.c. :        ARQMAANRTQIIAGWCVQRMQHGEQWAWMIVVLAAMLGQIGLPGGGFGFG
DorA/R.s. :        ARSFVAGRTMLAAGWSTQRMHHGEQAHWMLVTLASMIGQIGLPGGGFGLS


TorA/P.p. :        HFYSGVGLPFSTAAGPGGFPRNVDEGQQPIWNNNDLK---ATVRQFRSQD
TorA/S.m. :        HHYSSIGVPSSGAAAPGAFPRNLDENQKPLFDSSDFKGASSTIPVARWID
TorA/E.c. :        WHYNGAGTPGRKGVILSGFSGSTS--IPPVHDNSDYKGYSSTIPIARFID
DorA/R.s. :        YHYSNGGSPTSDGPALGGISDGGKAVEGAAWLSESGA---TSIPCARVVD


TorA/P.p. :        GLMRSSN
TorA/S.m. :        AILEPGKTIDANG
TorA/E.c. :        AILEPGKVINWNG
DorA/R.s. :        MLLNPGGEFQFNG
```

Figure 8

```
TorA/S.t. :  --------MKQVVSPQFEARNDFDIFRDLCRRFNREAAFTEGLDEMGWLK
TorA/E.c. :  ---RGIIAMKQVVPPQFEARNDFDIFRELCRRFNREEAFTEGLDEMGWLK
DorA/R.s. :  ---RAILAMKKVVDPLYEARSDYDIFAALAERLGKGAEFTEGRDEMGWIS
TorA/S.m. :  ---RGILAMQKMVEPLFDSLSDFEIFTRFAAVLGKEKEYTRNMGEMEWLE


TorA/S.t. :  RIWQEGSQQGKGRGIHLPIFEVFWNQQEYIEFDHPQ--MFVRHQAFREDP
TorA/E.c. :  RIWQEGVQQGKGRGVHLPAFDDFWNNKEYVEFDHPQ--MFVRHQAFREDP
DorA/R.s. :  SFYEAAVKQAEFKNVAMPSFEDFWSEG-IVEFPITEGANFVRYADFREDP
TorA/S.m. :  TLYNECKAANAGK-FEMPDFATFWKQG-YVHFGDGE--VWTRHADFRNDP


TorA/S.t. :  DLEPLGTPSGLIEIYSKTIADMQYDDGQGHPMWFEKIERSHGGPGSQRWP
TorA/E.c. :  DLEPLCTPSGLIEIYSKTIADMNYDDCQGHPMWFEKIERSHGGPGSQKYP
DorA/R.s. :  LFNPLGTPSGLIEIYSKNIEKMGYDDCPAHPTWMEPAER-LGGAG-AKYP
TorA/S.m. :  EINPLGTPSGLIEIFSRKIDQFGYDDCKGHPTWMEKTERSHGGPGSDKHP


TorA/S.t. :  LHLQSVHPDFRLHSQLLRV---------
TorA/E.c. :  LHLQSVHPDFRLHSQLCESETLRH----
DorA/R.s. :  LHVVASHPKSRLHSQLNGTSLRD-----
TorA/S.m. :  IWLQSCHPDKRLHSQMCESREYRE----
```
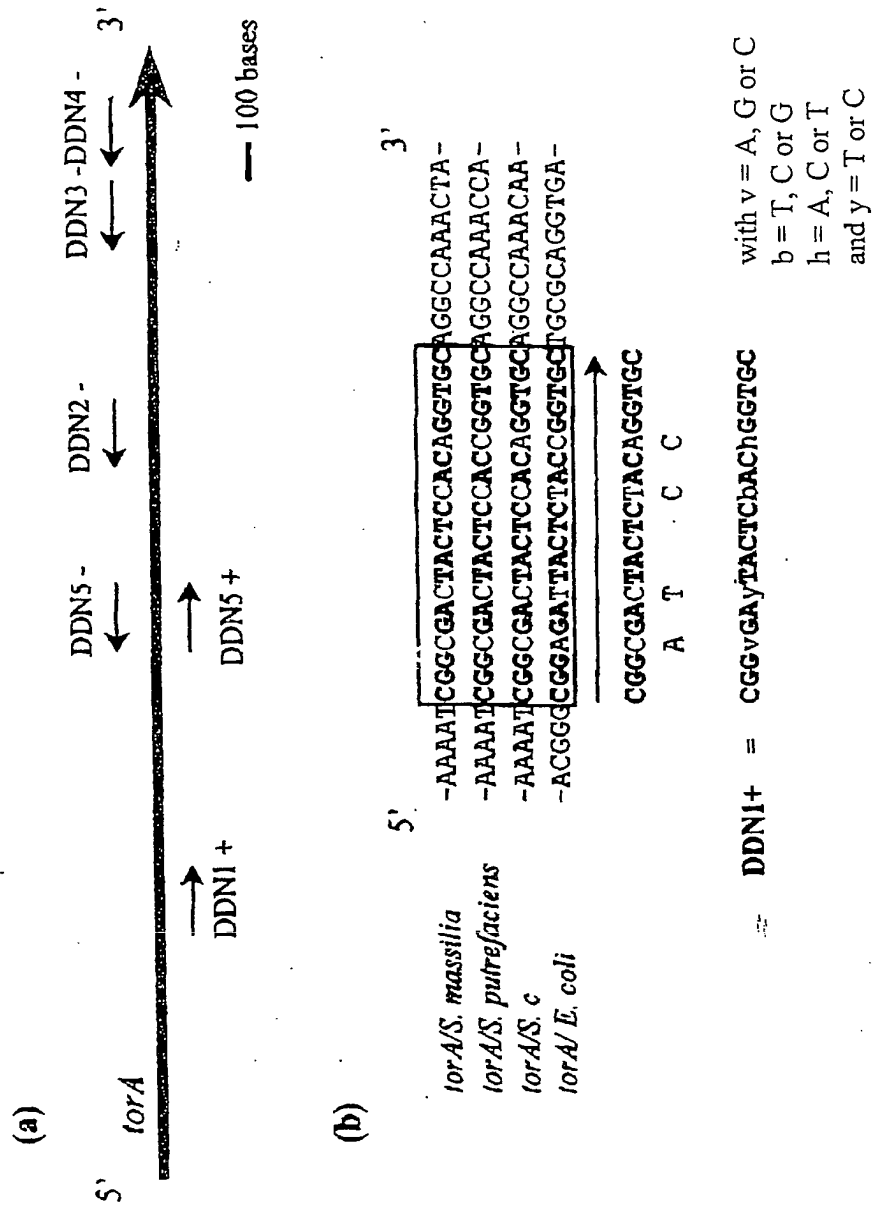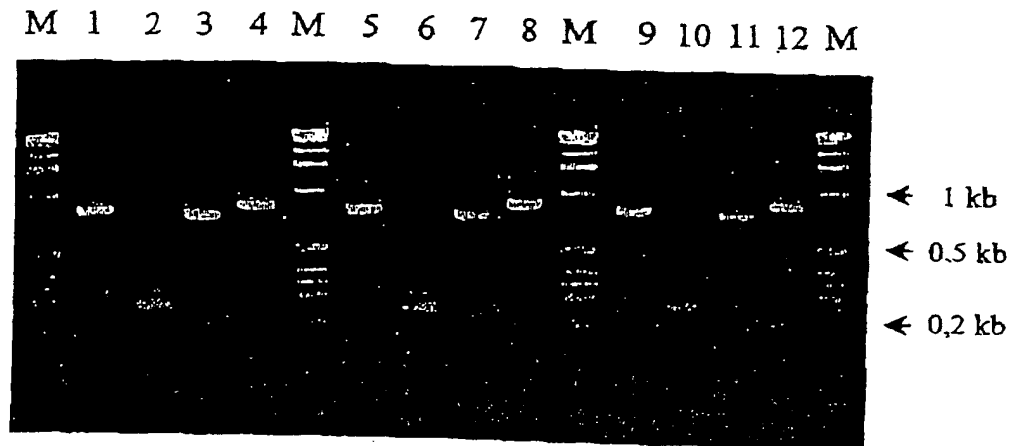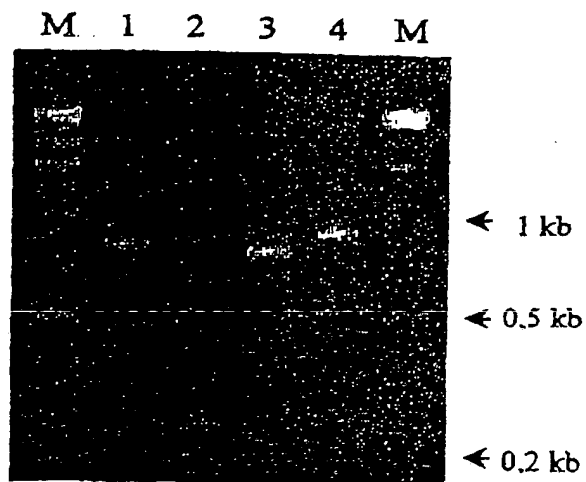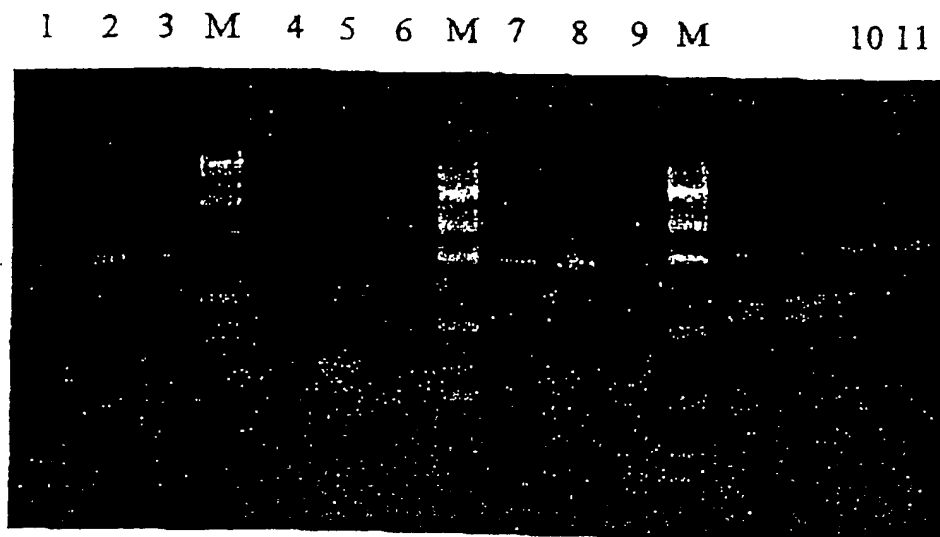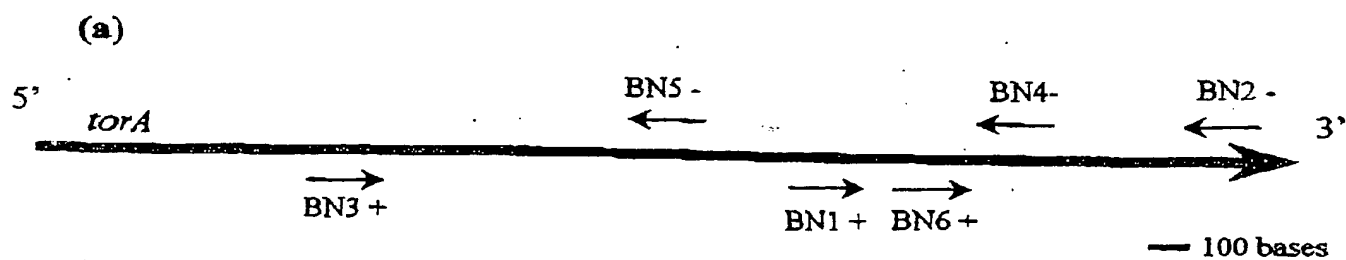
Figure 9

Figure 10

Figure 11

Figure 12

Figure 13

(a)

(b)

```
                        5'                                              3'
torA/S. massilia      -AAAATC GGCGACTACTCCACAGGTGC AGGCCAAACTA-
torA/ E. coli         -ACGGGC GGAGATTACTCTACCGGTGC AGGCCAAACCA-
dorA/R. sphaeroides   -TCGTCG GGCGACTATTCGACCGGCGC AGGCCAAACAA-
dorA/R.capsulatus     -GGCGCG GGCGATTATTCGACCGGCGC TGCGCAGGTGA-

                               GGCGACTATTCTACAGGCGC
                                A   T   C   C   C   T
                                                G
```

BN3+ = GGmGAyTAyTCbACmGGyGC   with m = A or C
                                        and y = T or C
                                        and b = T, C or G

Figure 14

TorC/S.m. : --------------MRKLTNLMRTLNKPTKALTLGAVSISAFIMGIIPWGGFNTALEATNTEAPCISCHSMESRPYQELQETVHWSNBFGVRATCPDCHVPHNW : 90
TorC/E.c. : --------------MRKLWNALRRPSARMSVLALVAIGIVIGIALIVLPHVGIKVTSTTBFCVSCHSMQP-VYEEYKQSVHFQNASGVRABCHDCHIPPDI : 86
DorC/R.s. : MGRSCGQASEAKVIGRIWKAEWRPSTKWGLGVLLVTGGLAGAVGWNGEHYVVEKTTTBFCISCHSMRDNNYEBYKTTIHYQNTSGVRABCADCHVPKSG : 100

                                                                          BC1+

TorC/S.m. : SRKIARGBASHDVAG-WLFNTVNTPBKFEAKRLEMASRBWKFDRDNSLACKNCHN-YNSMKWEAM-SPLAQKQMKRAAEIDQSCIDCHKGI-AHHLPE : 186
TorC/E.c. : PGMVKRKLBASNDIYCTFIAHSIDTPBKFEAKRABLAEREWARMKENNSATCRSCHN-YDAMDHAKQ-HPEAARQMKVAAKDNQSCIDCHKGI-AHQLPD : 183
DorC/R.s. : WKLYRAKLLAAKDLWG-EIRGTIDYTREKFEAHRLEMAETVWADMKQANDSATCRTCHS-EEAMDFAHQ-KPEASKQMQQAMNEGGTCIDCHKGI-AHKMPD : 196

                                                                          BC2+

TorC/S.m. : MGTARAPELIAEVGAGVSSVETN-QTYYSALTKPLFFTDKGDVE----AGTLNVATKVKVLETQGKRIKIGIDGWRKKIGAGR---VIYMDFGVNILSAQ : 278
TorC/E.c. : MSSGFRKQFDDVR-ASANDSG---DTLYSIDIKPIYAA-KGDKE---ASGSLLPASEVKVLKRDGDWLQIEITGWT--ESAGRQR-VLTQFPGKRIFVAS : 272
DorC/R.s. : MASGYRALFSKLEKASQSLKPRKGETLYPLRTIEAYLE-KPSGEKAKADGRLLAARTMQVVDVTGDMVYQVAVKGWQQ-EGAER---VIYEKQGKRIFNAA : 291

                                                                          BC3-

TorC/S.m. : LTKDAAETGGVIQTFEBKED----PMTGLKWQRTEAQIWTDKDYLLJTELQPLWGYARDTFRSSCSVCHTQPDEAHFDANTWPSMFQGMLAFVNMDQDTQAL : 375
TorC/E.c. : IRGDVQQQ----VKTLEKTTV---ADTNTEHSKLQATAWMKKGDWVNDIKPIWAYADSLYNGTCNQCHGAPEIAHFDANGWIGTLNGMIGFTSLDKREERT : 366
DorC/R.s. : LAPAATGS----VVPGASNVD---PDTEQTWTDVSLTARVRNRDLTGDQEALWQYGKQMYNGACGWCHVLPBPEHFLANQWIGTLNAMKSRAPLDDEQERL : 385

TorC/S.m. : VQKYLQEHSSTFVKKEH------- : 392
TorC/E.c. : LLKYLQMNASDTAGRAHGDKKEEK : 390
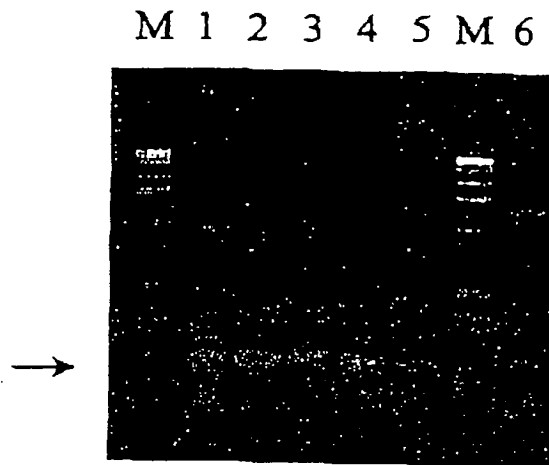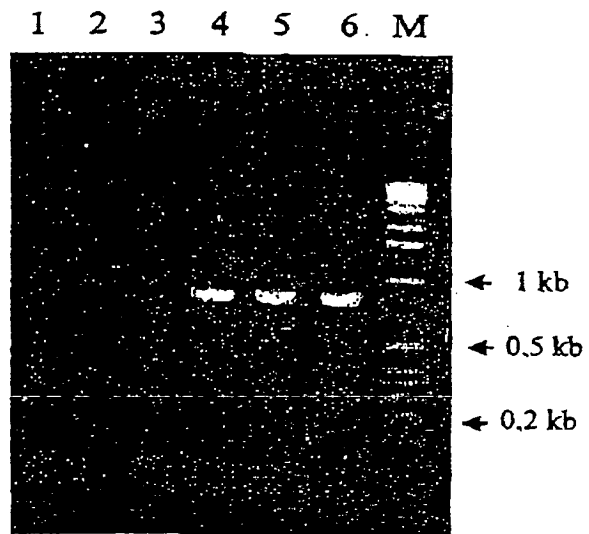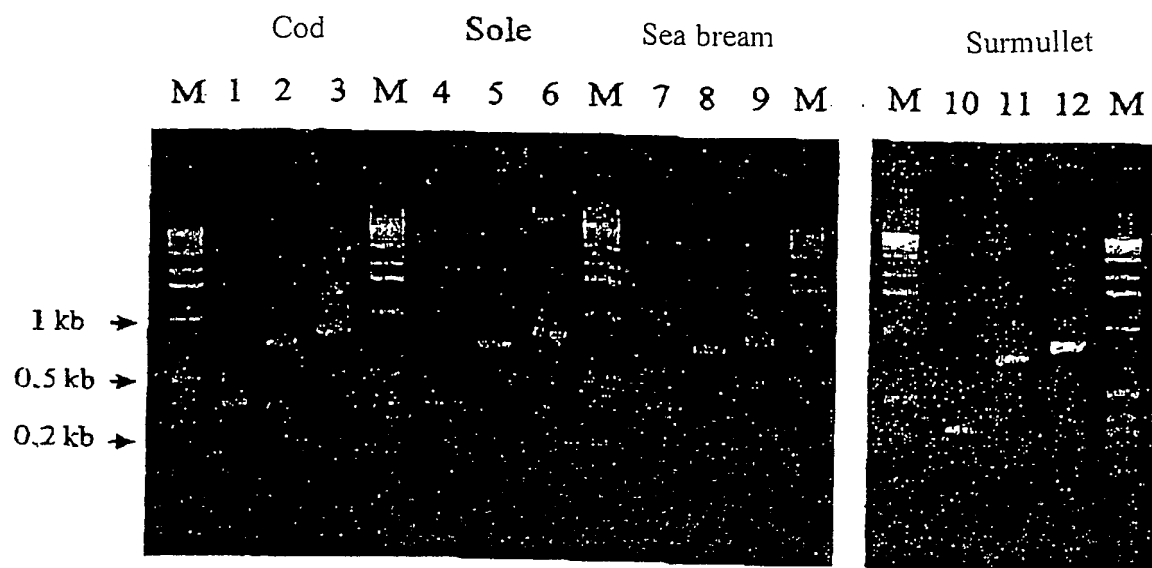DorC/R.s. : VQRYYQMHAKDVEPEGAAE----- : 404

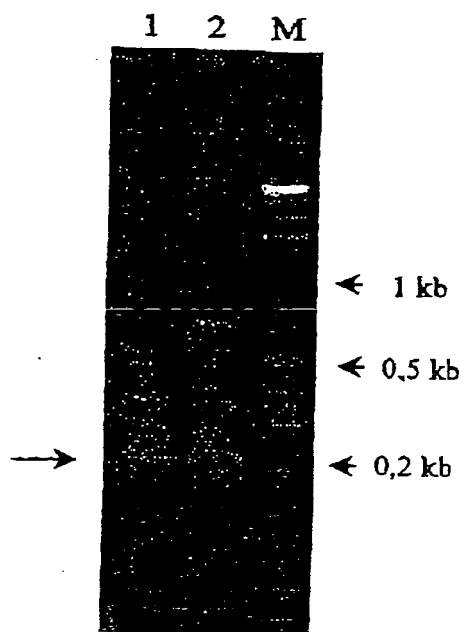Figure 15

Figure 16

Figure 17

Figure 18

Figure 19

Figure 19 (cont. 1)

torA/p.p.
torA/s.p.
torA/s.m.
torA/s.c
torA/s.t.

Figure 19 (cont. 2)

torA/p.p. :
torA/S.p. :
torA/S.m. :
torA/S.c :
torA/S.t. :

torA/p.p. :
torA/S.p. :
torA/S.m. :
torA/S.c :
torA/S.t. :

torA/p.p. :
torA/S.p. :
torA/S.m. :
torA/S.c :
torA/S.t. :

torA/p.p. :
torA/S.p. :
torA/S.m. :
torA/S.c :
torA/S.t. :

torA/p.p. :
torA/S.p. :
torA/S.m. :
torA/S.c :
torA/S.t. :

torA/p.p. :
torA/S.p. :
torA/S.m. :
torA/S.c :
torA/S.t. :

Figure 19 (cont. 3)